

Please cite:

```
/tmp/fastacaaOPaiHi: 995 aa
```

>SEO ID NO:2

```
vs /tmp/fastDAARPaHi library
```

```
searching /tmp/fastaDAARPaiHi library
```

1008 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2

```
join: 39, opt: 27, gap-pen: -12/-2, width: 16
```

Scan time: 0.050

The best scores are:

opt

NM\_000096 ACCESSION:NM\_000096 NID: gi 4557484 ref (1008) 2671

>>NM\_000096 ACCESSION:NM\_000096 NID: gi 4557484 ref NM\_0 (1008 aa)

```
initn: 1414  init1: 972  opt: 2671
```

Smith-Waterman score: 3980; 57.002% identity in 1014 aa overlap (1-992:1-1008)

```

          10          20          30          40          50
SEQ      MKILILGIFLFLCSPGWAIDRHCYIGIEESIWNYPAPSGKNMLNEKPFSEDL-----FLQ
          ::::::::::::::: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
NM_000    MKILILGIFLFLCSTPAWAKEKHYYIGIETTDWYA--SDHGEKKLISVDTEHSNIYLQ
          10          20          30          40          50

```

```

      60          70          80          90         100         110
SEQ      GGQARKSFVFKKALYFQYTDNTFQRRIIEKPSWLGLGPMIKAETGDFIYVHVKNNASRAY
        . :   . :   . :   . :   . :   . :   . :   . :   . :   . :   . :
NM_000    NGPDRIGRLYKKALYLQYTDDETFRTTIEKPVLGLGPPIKAETGDKVYVHLKNLASRPY
      60          70          80          90         100         110

```

	120	130	140	150	160	170
SEQ	SYHPHGLTYSKENEAHGAIYPDNTTGLQKEVEYLEPGKQYTYKWYVEEHQGGPNDNSNCV					
	..	..	..	..	..	..
NM_000	TFHSHGITYYKEHE--GAIYPDNTTDFQRADDKVYPGEQYTYMLLATEEQSPGEGDGNVCV					
	120	130	140	150	160	170

	180	190	200	210	220	230
SEQ	TRIYHSHIDTARDVASGLIGPILTCRGT	LN	GDTEK	IDRSSFL	MFSTTDES	RSWYSDEN
	.....	.....	..	..	::	..... :: ..
NM_000	TRIYHSHIDAPKD	IASGLIGPL	IICKDS	LDKEKEKH	IDREFVVM	FSVVDFNSWYLEDN
	180	190	200	210	220	230

	240	250	260	270	280	290
SEQ	IRAF-TESGKINTSDPRFEESMSMQSINGYIYGNLPNLT	MCAEDRVQWYFVGMGGVADIH				
	...	:	...	.	:	:
	:	:	:	:	:	:
NM_000	IKTYCSEPEKVDKDNE	DFQESNRMYSVNGYTFGSLPGLSMCAEDRVKWYLF	GMGNEVDVH			
	240	250	260	270	280	290

```

          300          310          320          330          340          350
SEQ      PVYLRGQTLISRNHRKDTIMLFPSSEDAFMVAKAPGVWMLGCQ----IHESMQAFFKVS
          .....:::.....:.....:.....:.....:.....:.....:.....:.....
NM_000    AAFHHGQALTNKNYRIDTINLFPATLFDAYMVAQNPGEWMLSCQNLNHLKAGLQAFFQVQ
          300          310          320          330          340          350

```

	360	370	380	390	400	410
SEQ	NCQKPSTEAFVTGTHVIHYIIAAKEILWNYAPSGIDFFTKKNLTAAGSKSQLFFERSPTR					
	....	...	.	:	:	.....
NM_000	ECNKSSSKDNIRGKHVRHYIIAAEEIIWNYAPSGIDIFTKENLTAPGSDSAVFFEQGTTR					
	360	370	380	390	400	410

  

	420	430	440	450	460
SEQ	IGGTYKKLIYREYTDASFQTQKAR---EEHLGILGPVFKAEVQGTIKITFYNNASLPLSI				
	.....	...	:	:	.....
NM_000	IGGSYKKLVYREYTDASFQTNRKERGPEEEHLGILGPVIWAEVGDITRVTFHNKGAYPLSI				
	420	430	440	450	460

  

	470	480	490	500	510	520
SEQ	QPPGLHYNKSNEGLFYE---TPGG-STPPPSHHVSPGTTFVYTWEVPKDVGPTSTDPNCL					
	..	.....	:	:	.....	:
NM_000	EPIGVRFNKNNEGTYYSPPNYNPQSRVPPSASHVAPTETFTYEWTVPKEVGPTNADPVCL					
	480	490	500	510	520	530

  

	530	540	550	560	570	580
SEQ	TWFFYSSVNGKKDINSGLLGPLLICRNGSLGDDGKQKGVDFEYLLATIFDENESNLLDE					
	.	.....	:	:	.....	:
NM_000	AKMYSAVDPTKDIPTGLIGPMKICKKGSLSHANGRQKDVDFEYLLPTVFDENESLLED					
	540	550	560	570	580	590

  

	590	600	610	620	630	640
SEQ	N-RTFITEPENIDKEDTDCQASNKMYSSINGMYGNLPGLDTCLGDNVLWHVFSVGSVEDL					
	:	:	:	:	:	:
NM_000	NIRMFTTAPDQVDKEDEDFQESNKMMSMNGFMYGNQPGGLTMCKGDSVVWYLFSAAGNEADV					
	600	610	620	630	640	650

  

	650	660	670	680	690	700
SEQ	HGIYFSGNTFTSLGARRDTIPMFYTSQTLLMTPDSIGTFDLVCMTIKHNLGGMKHKYHV					
	.....	:	:	:	:	:
NM_000	HGIYFSGNTYLRGERRDTANLFPQTSLLHMPDTEGTFNVECLTTDHYTGGMKQKYTV					
	660	670	680	690	700	710

  

	710	720	730	740	750	760
SEQ	RQCGKPNPDQTYQEEKIIITIAAEEMEWYDYSRKRWENELHHLRRENQTSMYVDRSGTL					
	:	:	:	:	:	:
NM_000	NQCRQSEDSTFYLGERTYY-IAAVEVEWYDYSQREWEKELHHLQEQNVSNFLDKGEFY					
	720	730	740	750	760	770

  

	770	780	790	800	810	820
SEQ	LGSKYKKVLYRQYDDNTFTNQTKRNEGEKHLDDLGLILLNPGQIIQIIFKNKAARPYSI					
	.....	:	:	:	:	:
NM_000	IGSKYKKVVYRQYTDSTFRVPVERKAEEEHLGILGPQLHADVGDKVKIIFKNMATRPYSI					
	780	790	800	810	820	830

  

	830	840	850	860	870	880
SEQ	HAHGVTNNSTVVPTQPGEIQIYTQIPDRGTSLDFECIPWFYYSTVSVAKDLHSGLV					
	.....	:	:	:	:	:
NM_000	HAHGVTQTESSTVTPPLPGETLTYVWKIPERSGAGTEDSACIPWAYYSTVDQVKDLYSGLI					
	840	850	860	870	880	890

```

      890          900          910          920          930
SEQ    GPLSVCR----KDINPN-IVHRVLHFMIFDENESWYFEDSINTYASKPNKVVDKENDNFQL
      ::: :::   :  :::   ..  .:  ::::::::::::::::::::::::::::::::::::
NM_000  GPLIVCRRPYLKVFNP RRKLEFALLFLVFDENESWYLD DNIKTYS DHPEKVNKDDEEFIE
      900          910          920          930          940          950

      940          950          960          970          980          990
SEQ    SNQMHAINGRLFGNNQGITFHVGDVVNWYLI GIGNEADLHTVHFHGH SFEYKHKYLI
      :::::::::::::: :::::::::: :::::::::::::: ::::::::::::::::::::
NM_000  SNKMHAINGRMFGNLQGLTMHVGDEVNWYLMGMGNEIDLHTVHFHGH SFQYKHR
      960          970          980          990          1000

```

995 residues in 1 query sequences

1008 residues in 1 library sequences

Scomplib [version 3.3t05 March 30, 2000]

start: Wed Sep 18 11:16:31 2002 done: Wed Sep 18 11:16:32 2002

Scan time: 0.050 Display time: 1.417

Function used was FASTA